

FIG.1

1 CTTTCATACC GGCCCTTCCC CTCGGCTTTG CCTGGACAGC TCCTGCCTCC GGCAGGGCCC
 61 ACCTGTGTCC CCCAGCGCCG CTCACCCAG CAGGCCTGAG CCCCTCTCTG CTGCCAGACA
 121 CCCCTGCTG CCCACTCTCC TGCTGCTCGG GTTCTGAGGC ACAGCTTGTG ACACCGAGGC
 181 GGATTCTCTT TCTCTTTCTC TTCTGGCCCA CAGCCGCAGC AATGGCGCTG AGTTCCTCTG
 241 CTGGAGTTCA TCCTGCTAGC TGGGTTCCCG AGCTGCCGGT CTGAGCTGA GGCATGGAGC
 M E

 301 CTCCTGGAGA CTGGGGGCCT CCTCCCTGGA GATCCACCCC CAGAACCAGC GTCTTGAGGC
 P P G D W G P P P W R S T P R T D V L R

 361 TGGTGCTGTA TCTCACCTTC CTGGGAGCCC CCTGCTACGC CCCAGCTCTG CCGTCTGCA
 L V L Y L T F L G A P C Y A P A L P S C

 421 AGGAGGACGA GTACCCAGTG GGCTCCGAGT GCTGCCCAA GTGCAGTCCA GGTTATCGTG
 K E D E Y P V G S E C C P K C S P G Y R

 481 TGAAGGAGGC CTGCGGGGAG CTGACGGGCA CAGTGTGTGA ACCCTGCCCT CCAGGCACCT
 V K E A C G E L T G T V C E P C P P G T

 541 ACATTGCCCA CCTCAATGGC CTAAGCAAGT GTCTGCAGTG CCAAATGTGT GACCCAGCCA
 Y I A H L N G L S K C L Q C Q M C D P A

 601 TGGGCCTGCG CGCGAGCCGG AACTGCTCCA GGACAGAGAA CGCGTGTGTG GGCTGCAGCC
 M G L R A S R N C S R T E N A V C G C S

 661 CAGGCCACTT CTGCATCGTC CAGGACGGGG ACCACTGCGC CGCGTGCCGC GCTTACGCCA
 P G H F C I V Q D G D H C A A C R A Y A

 721 CCTCCAGCCC GGGCCAGAGG GTGCAGAAGG GAGGCACCGA GAGTCAGGAC ACCCTGTGTC
 I S S P G Q R V Q K G G T E S Q D T L C

 781 AGAACTGCCC CCCGGGGACC TTCTCTCCCA ATGGGACCTT GGAGGAATGT CAGCACCAGA
 Q N C P P G T F S P N G T L E E C Q H Q

 841 CCAAGTGCAG CTGGCTGGTG ACGAAGGCCG GAGCTGGGAC CAGCAGCTCC CACTGGGTAT
 I K C S W L V T K A G A G T S S S H W V

 901 GGTGGTTTCT CTGAGGGAGC CTCGTATCGT TCATTGTTTG CTCCACAGTT GGCCTAATCA
 W W F L S G S L V I V I V C S T V G L I

FIG.2A

961 TATGTGTGAA AAGAAGAAAG CCAAGGGGTG ATGTAGTCAA GGTGATCGTC TCCGTCCAGC
I C V K R R K P R G D V V K V I V S V Q
 1021 GGAAAAGACA GGAGGCAGAA GGTGAGGCCA CAGTCATTGA GGCCCTGCAG GCCCCTCCGG
 R K R Q E A E G E A T V I E A L Q A P P
 1081 ACGTCACCAC GGTGGCCGTG GAGGAGACAA TACCCTCATT CACGGGGAGG AGCCCAAACC
 D V T T V A V E E T I P S F T G R S P N
 1141 ACTGACCCAC AGACTCTGCA CCCCAGCGCC AGAGATACCT GGAGCGACGG CTGCTGAAAG
 H -
 1201 AGGCTGTCCA CCTGGCGAAA CCACCGGAGC CCGGAGGCTT GGGGGCTCCG CCCTGGGCTG
 1261 GCTTCCGTCT CCTCCAGTGG AGGGAGAGGT GGGGGCCCTG CTGGGGTAGA GCTGGGGACG
 1321 CCACGTGCCA TTCCCATGGG CCAGTGAGGG CTTGGGGCCT CTGTTCTGCT GTGGCCTGAG
 1381 CTCCCCAGAG TCCTGAGGAG GAGCGCCAGT TGCCCTCGC TCACAGACCA CACACCCAGC
 1441 CCTCCTGGGC CAGCCCAGAG GGCCCTTCAG ACCCCAGCTG TCTGCGCGTC TGA CTCTTGT
 1501 GGCTCAGCA GGACAGGCC CGGGCACTGC CTCACAGCCA AGGCTGGACT GGGTTGGCTG
 1561 CAGTGTGGTG TTTAGTGGAT ACCACATCGG AAGTGATTTT CTAAATTGGA TTTGAATTCC
 1621 GGTCTGTCT TCTATTTGTC ATGAAACAGT GTATTTGGGG AGATGCTGTG GGAGGATGTA
 1681 AATATCTTGT TTCTCTCAA AAAAAAAAAA AAAAAAAAAA AAAA

FIG.2B

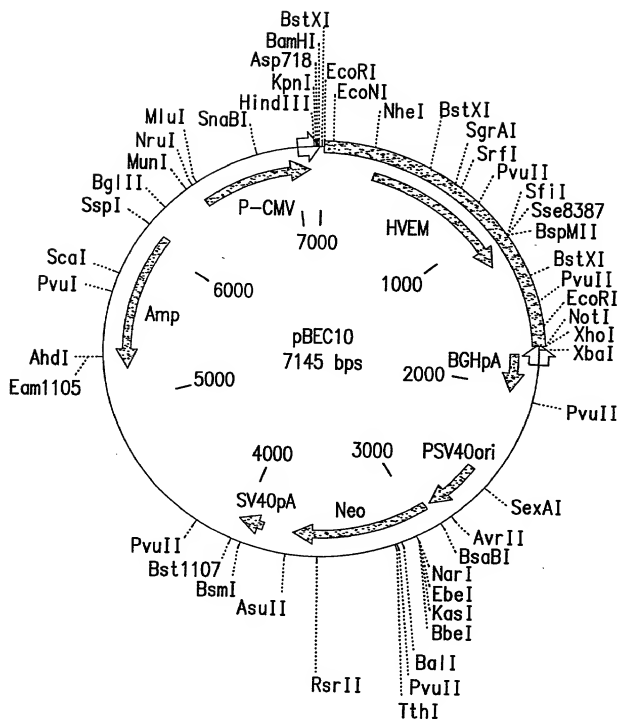


FIG.3

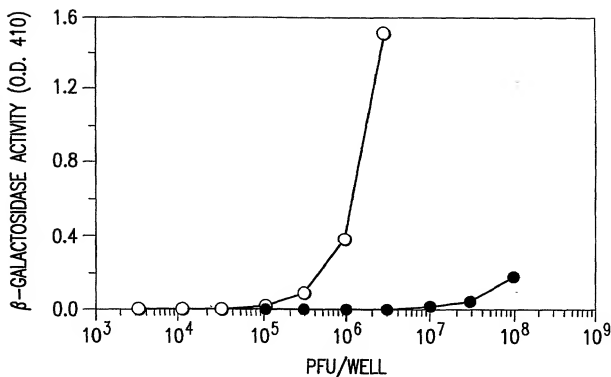


FIG. 4A

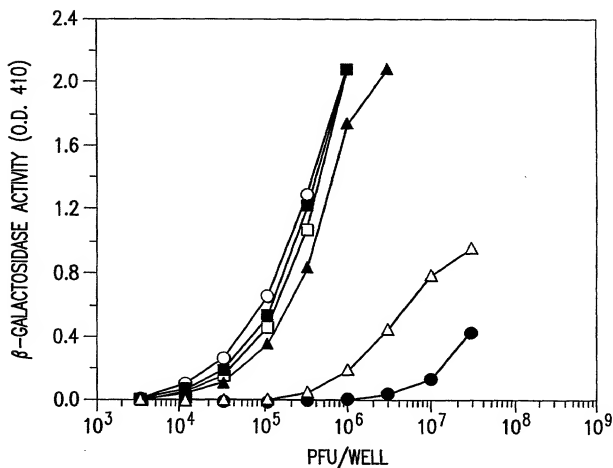


FIG. 4B

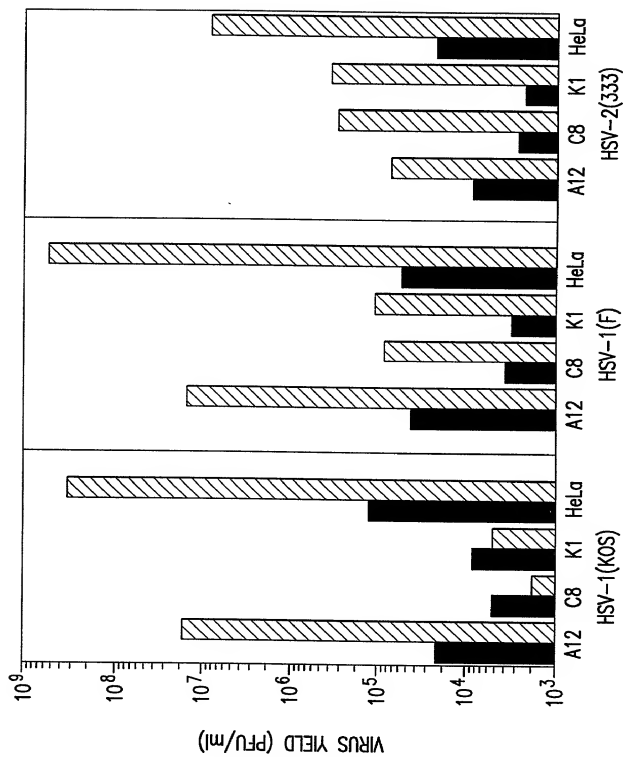


FIG.5

gD-1 AND gD-2 INTERFERE WITH KOS(gL86) INFECTION OF A12 CELLS

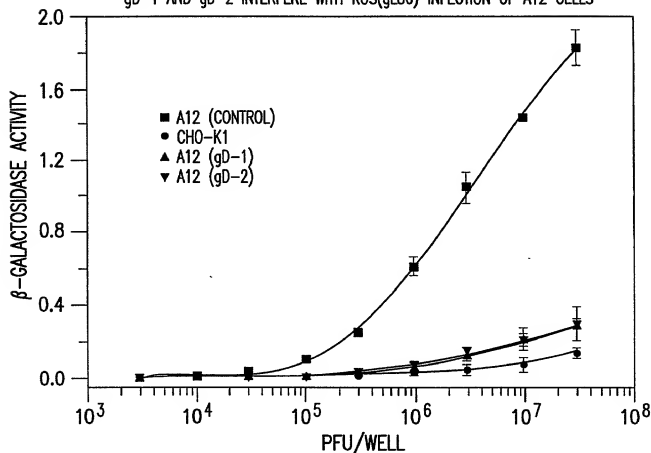


FIG. 6A

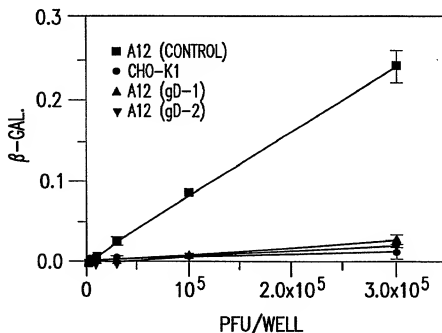


FIG. 6B

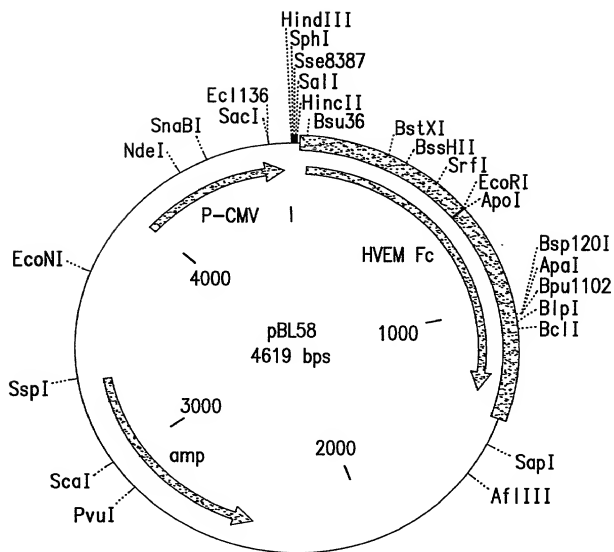


FIG.7

1 AAGCTTGCAT GCCTGCAGGT CGACTCTAGC TGGGTTCCCG AGCTGCCGGT CTGAGCCCTGA
 61 GGCATGGAGC CTCCTGGAGA CTGGGGGCTT CCTCCCTGGA GATCCACCCC CAGAACCAGC
 M E P P G D W G P P P W R S T P R T D

 121 GTCTTGAGGC TGGTGCTGTA TCTCACCTTC CTGGGAGCCC CCTGCTACGC CCCAGCTCTG
 V L R L V L Y L T F L G A P C Y A P A L

 181 CCGTCTGCA AGGAGGACGA GTACCCAGTG GGCTCCGAGT GCTGCCCCAA GTGCAGTCCA
 P S C K E D E Y P V G S E C C P K C S P

 241 GGTATCGTG TGAAGGAGGC CTGCGGGGAG CTGACGGGCA CAGTGTGTGA ACCCTGCCCT
 G Y R V K E A C G E L T G T V C E P C P

 301 CCAGGCACCT ACATTGCCCA CCTCAATGGC CTAAGCAAGT GTCTGCAGTG CCAATGTGT
 P G T Y I A H L N G L S K C L Q C Q M C

 361 GACCCAGCCA TGGGCCTGCG CGCGAGCCGG AACTGTCTCA GGACAGAGAA CGCCGTGTGT
 D P A M G L R A S R N C S R T E N A V C

 421 GGCTGCAGCC CAGGCCACTT CTGCATCGTC CAGGACGGGG ACCACTGCGC CGCGTGCCGC
 G C S P G H F C I V Q D G D H C A A C R

 481 GCTTACGCCA CCTCCAGCCC GGGCCAGAGG GTGCAGAAGG GAGGCACCGA GAGTCAGGAC
 A Y A T S S P G Q R V Q K G G T E S Q D

 541 ACCCTGTGTC AGAACTGCCC CCCGGGGACC TTCTCTCCCA ATGGGACCCT GGAGGAATGT
 I L C Q N C P P G T F S P N G T L E E C

 601 CAGCACCAGA CCAAGTGCAG AATTACAAG ACCGTTGCAC CCTCGACATG CAGCAAGCCC
 Q H Q T K C R I H K T V A P S T C S K P

 661 ACGTGCCAC CCCCTGAACT CCTGGGGGGA CCGTCTGTCT TCATCTTCCC CCCAAAACCC
 T C P P P E L L G G P S V F I F P P K P

 721 AAGGACACCC TCATGATCTC ACGCACCCCC GAGGTACAT GCGTGGTGGT GGACGTGAGC
 K D T L M I S R T P E V T C V V V D V S

 781 CAGGATGACC CCGAGGTGCA GTTCACATGG TACATAAACA ACGAGCAGGT GCGCACCGCC
 Q D D P E V Q F T W Y I N N E Q V R T A

FIG.8A

841 CGGCCGCCG TACGGGAGCA GCAGTTCAAC AGCAGCATCC GCGTGGTCAG CACCCTCCCC
 R P P L R E Q Q F N S T I R V V S T L P
 901 ATCACGCACC AGGACTGGCT GAGGGCAAG GAGTTCAAGT CAAAGTCCA CAACAAGGCA
 I T H Q D W L R G K E F K C K V H N K A
 961 CTCCCGGCC CCATCGAGAA AACCATCTCC AAAGCCAGAG GGCAGCCCCT GGAGCCGAAG
 L P A P I E K T I S K A R G Q P L E P K
 1021 GTCTACACCA TGGGCCCTCC CCGGGAGGAG CTGAGCAGCA GGTGCGTCAG CCTGACCTGC
 V Y T M G P P R E E L S S R S V S L T C
 1081 ATGATCAACG GCTTCTACCC TTCCGACATC TCGGTGGAGT GGGAGAAGAA CGGGAAGGCA
 M I N G F Y P S D I S V E W E K N G K A
 1141 GAGGACAAC AACAAGACCAC GCCGGCCGTG CTGGACAGCG ACGGCTCCTA CTTCTCTAC
 E D N Y K T T P A V L D S D G S Y F L Y
 1201 AACAACTCT CAGTGCCAC GAGTGAGTGG CAGCGGGGCG ACGTCTTCAC CTGCTCCGTG
 N K L S V P T S E W Q R G D V F T C S V
 1261 ATGCACGAGG CCTTGCACAA CCACTACACG CAGAAGTCCA TCTCCCGCTC TCCGGGTAAA
 M H E A L H N H Y T Q K S I S R S P G K
 1321 TGAGCGCTGT GCCGCGGAGC TGCCCCCTCT CCTCCCCCCC ACGCCGACG TGTGACCCCC
 1381 GCACACAAT AAAGCACCCA GCTCTGCCCT GAACAGCTTC CGGTCTCCCT ATAGTGAGTC
 1441 GTATTAATTT CGATAAGCCA GCTGCATTAA TGAATCGGCC AACCGCGGG GAGAGGCGGT
 1501 TTGCGTATTG GGCCTCTTC CGCTTCCTCG CTCAGTACT CGTGCGCTC GGTCGTTCCG
 1561 CTGCGGCGAG CGGTATCAGC TCACTCAAG GCGTAATAC GGTATCCAC AGAATCAGGG
 1621 GATAACGCAG GAAAGAACAT GTGAGCAAAA GGCCAGCAAA AGGCCAGGAA CCGTAAAAAG
 1681 GCCGCGTTGC TGGCGTTTTT CCATAGGCTC CGCCCCCTG ACGAGCATCA CAAAAATCGA
 1741 CGCTCAAGTC AGAGGTGGCG AAACCCGACA GGAATAAAA GATACCAGGC GTTTCCTCCT
 1801 GGAAGCTCCC TCGTGCGCTC TCCTGTTCCG ACCCTGCCGC TTACCGGATA CCTGTCCGCC
 1861 TTTCTCCCTT CCGGAAGCGT GGCCTTTCT CATAGCTCAC GCTGTAGGTA TCTCAGTTCC
 1921 GTGTAGGTG TTCGCTCCAA GCTGGGCTGT GTGCAGGAAC CCCCCTGTTA GCCCGACCGC
 1981 TGCGCCTTAT CCGGTAACCTA TCGTCTTGAG TCCAACCCGG TAAGACACGA CTTATCGCCA
 2041 CTGGCAGCAG CCACTGGTAA CAGGATTAGC AGAGCAGAGT ATGTAGGCGG TGCTACAGAG
 2101 TTCTTGAAGT GGTGGCTAA CTACGGCTAC ACTAGAAGGA CAGTATTTGG TATCTCGCT
 2161 CTGCTGAAGC CAGTTACCTT CGGAAAAAGA GTTGGTAGCT CTTGATCCCG CAAACAACCC
 2221 ACCGCTGGTA GCGGTGGTTT TTTTGTGTC AAGCAGCAGA TTACGCGCAG AAAAAAAGGA

FIG.8B

2281 TCTCAAGAAG ATCCTTTGAT CTTTTCTACG GGGTCTGACG CTCAGTGGAA CGAAAACCTCA
 2341 CGTTAAGGGA TTTTGGTCAT GAGATTATCA AAAAGGATCT TCACCTAGAT CCTTTTAAAT
 2401 TAAAAATGAA GTTTTAAATC AATCTAAAGT ATATATGAGT AAACCTTGGTC TGACAGTTAC
 2461 CAATGCTTAA TCAGTGAGGC ACCTATCTCA GCGATCTGTC TATTTCTGTC ATCCATAGTT
 2521 GCCTGACTCC CCGTCGTGTA GATAACTACG ATACGGGAGG GCTTACCATC TGGCCCCAGT
 2581 GCTGCAATGA TACCGCGAGA CCCACGCTCA CCGGCTCCAG ATTTATCAGC AATAAACCCAG
 2641 CCAGCCGGAA GGGCCGAGCG CAGAAGTGGT CCTGCAACTT TATCCGCCCT CACTCCAGTCT
 2701 ATTAATTGTT GCCGGGAAGC TAGAGTAAGT AGTTCGCCAG TTAATAGTTT GCGCAACGTT
 2761 GTTGCCATTG CTACAGGCAT CGTGGTGTC ACGTCGTCGT TTGGTATGGC TTCATTGAGC
 2821 TCCGGTTCCC AACGATCAAG GCGAGTTACA TGATCCCCCA TGTTGTGCAA AAAAGCGGTT
 2881 AGCTCCTTCG GTCTCCCGAT CGTTGTGAGA AGTAAGTTGG CCGCAGTGTT ATCACTCATG
 2941 GTTATGGCAG CACTGCATAA TTCTCTTACT GTCATGCCAT CCGTAAGATG CTTTTCTGTG
 3001 ACTGGTGAGT ACTCAACCAA GTCATTCTGA GAATAGTGTA TCGCGCGACC GAGTTGCTCT
 3061 TGCCCCGGCT CAATACGGGA TAATACCGCG CCACATAGCA GAACTTTAAA AGTGCTCATC
 3121 ATTGAAAAC GTCTCTCGGG GCGAAAACTC TAAGGATCT TCCCGCTGTT ATCGGTCAGT
 3181 TCGATGTAAC CCACTCGTGC ACCCAACTGA TCTTCAGCAT CTTTACTTTT CACCAGCGTT
 3241 TCTGGGTGAG CAAAACAGG AAGGCAAAAT GCCGCAAAA AGGGAATAAG GGCACACGG
 3301 AAATGTTGAA TACTCATACT CTTCTTTTTT CAATATTATT GAAGCATTTA TCAGGGTTAT
 3361 TGTCTCATGA GCGGTACAT ATTTGAATGT TTTTAGAAAA ATAAACAAAT AGGGTTCGCG
 3421 CGCACATTTT CCCGAAAAGT GCCACCTGAC GTCTAAGAAA CCATTATTAT CATGACATTA
 3481 ACCTATAAAA ATAGGCGTAT CACGAGGCC TTTCTGTCG CGCGTTTCGG TGATGACGGT
 3541 GAAAACCTCT GACACATGCA GCTCCCGGAG ACGGTACAGC CTGTGCTGTA AGCGGATGCC
 3601 GGGAGCAGAC AAGCCCGTCA GGGCGCGTCA GCGGGTGTTG GCGGGTGTCG GGGCTGGCTT
 3661 AACTATGCGG CATCAGAGCA GATTGTACTG AGAGTGCACC ATATCGACGC TCTCCCTTAT
 3721 GCGACTCCTG CATTAGGAAG CAGCCAGTA GTAGGTTGAG GCCGTTGAGC ACCGCCGCCG
 3781 CAAGGAATGG TGCAAGGAGA TGGCGCCCAA CAGTCCCCCG GCCACGGGGC CTGCCACCAT
 3841 ACCCAGCCG AAACAAGCGC TCATGAGCCC GAAGTGGCGA GCCGATCTTT CCCCATCGST
 3901 GATGTCGGCG ATATAGGCGC CAGCAACCGC ACCTGTGGCG CCGGTGATGC CGGCCACGAT
 3961 GCGTCCGGCG TAGAGGATCT GGCTAGTTAT TAATAGTAAT CAATTACGGG GTCATTAGTT
 4021 CATAGCCCAT ATATGGAGTT CCGCGTTACA TAACCTACGG TAAATGGCCC GCCTGGCTGA
 4081 CCGCCCAACG ACCCCGCCC ATTGACGTCA ATAATGACGT ATGTTCCCAT AGTAACGCCA
 4141 ATAGGGACTT TCCATTGACG TCAATGGGTG GACTATTTAC GGTAAACTGC CCACTTGGCA
 4201 GTACATCAAG TGTATCATAT GCCAAGTACG CCCCCTATTG ACGTCAATGA CGGTAATAGG
 4261 CCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT TTCTACTTTG GCAGTACATC
 4321 TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT GGCAGTACAT CAATGGGCGT
 4381 GGATAGCGGT TTGACTCAGC GGGATTTCCA AGTCTCCACC CCATTGACGT CAATGGGAGT
 4441 TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC GTAAACAACCT CGCCCCATTG
 4501 ACGCAAATGG CGGGTAGGCG TGTACGGTGG GAGGTCTATA TAAGCAGAGC TCTCTGGCTA
 4561 ACTAGAGAAC CCACTGCTTA ACTGGCTTAT CGAAATTAAT ACGACTCAAT ATAGGGAGAC
 4621 CC

FIG.8C

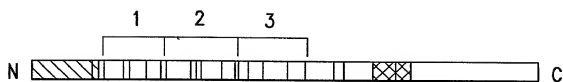


FIG.9

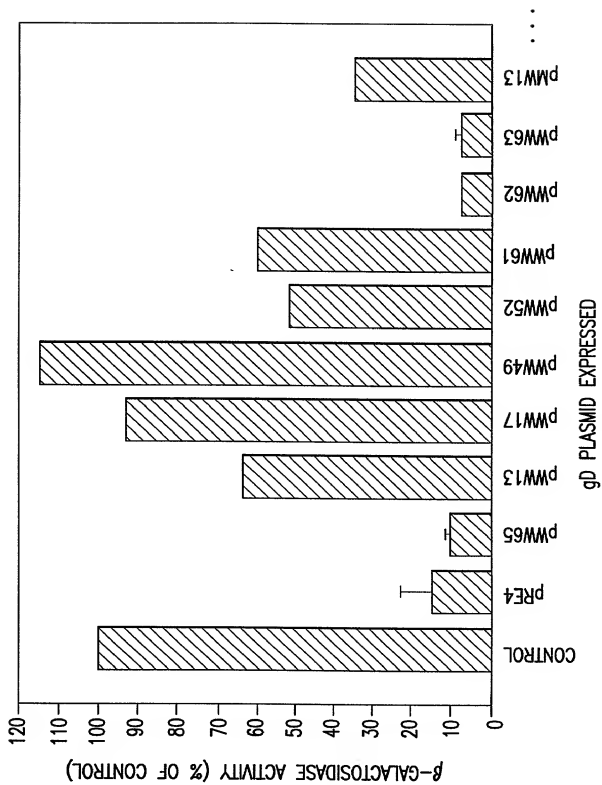


FIG.10